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OIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/855,604

DATE: 05/14/2002
 TIME: 16:01:50

#14

Input Set : D:\37156201.app
 Output Set: N:\CRF3\05142002\I855604.raw

P.6

ENTERED

RECEIVED

JUN 04 2002

OFFICE OF PETITIONS

3 <110> APPLICANT: GICQUEL, BRIGITTE
 4 PORTNOI, DENIS
 5 LIM, ENG-MONG
 6 PELICIC, VLADIMIR
 7 GUIGUENO, AGNES
 8 GOGUET DE LA SALMONIERE, YVES
 10 <120> TITLE OF INVENTION: POLYPEPTIDE NUCLEIC SEQUENCES EXPORTED FROM MYCOBACTERIA,
 11 VECTORS COMPRISING SAME AND USES FOR DIAGNOSING AND
 12 PREVENTING TUBERCULOSIS
 14 <130> FILE REFERENCE: 03715.0062-01000
 16 <140> CURRENT APPLICATION NUMBER: 09/855,604
 17 <141> CURRENT FILING DATE: 2001-05-16
 19 <150> PRIOR APPLICATION NUMBER: 09/485,536
 20 <151> PRIOR FILING DATE: 2000-02-14
 22 <150> PRIOR APPLICATION NUMBER: PCT/FR98/01813
 23 <151> PRIOR FILING DATE: 1998-08-14
 25 <150> PRIOR APPLICATION NUMBER: FR 97 10404
 26 <151> PRIOR FILING DATE: 1997-08-14
 28 <150> PRIOR APPLICATION NUMBER: FR 97 11325
 29 <151> PRIOR FILING DATE: 1997-09-11
 31 <160> NUMBER OF SEQ ID NOS: 935
 33 <170> SOFTWARE: PatentIn Ver. 2.1
 35 <210> SEQ ID NO: 1
 36 <211> LENGTH: 1243
 37 <212> TYPE: DNA
 38 <213> ORGANISM: Mycobacterium tuberculosis
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 41 <221> NAME/KEY: CDS
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 44 <220> FEATURE:
 45 <221> NAME/KEY: CDS
 46 <222> LOCATION: (124)..(453)
 48 <220> FEATURE:
 49 <221> NAME/KEY: CDS
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 52 <220> FEATURE:
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 56 <220> FEATURE:
 57 <221> NAME/KEY: CDS
 58 <222> LOCATION: (719)..(928)
 60 <220> FEATURE:
 61 <221> NAME/KEY: CDS

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62 <222> LOCATION: (942)..(1241)
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65 ggatcccagg gaacgtgacc atg gtc gta ggg atg act tgacagtttc 48
66 Met Val Val Gly Met Thr
67 1 5
69 aacgggggtgc gaccaccgtt gcgctcagaa ggcatacggtt ggtggaacac gtcggaagc 108
71 tgggaggtga atctg atg gct ggc gac caa gag ctg gaa ctg cgg ttc gac 159
72 Met Ala Gly Asp Gln Glu Leu Glu Leu Arg Phe Asp
73 10 15
75 gtt cct ctt tac acg ctt gcc gag gca tcg cgg tac ctg gtg gtt ccc 207
76 Val Pro Leu Tyr Thr Leu Ala Glu Ala Ser Arg Tyr Leu Val Val Pro
77 20 25 30
79 cgc gcc acc ctg gct acg tgg gct gac ggc tac gag cgt cgg ccg gcc 255
80 Arg Ala Thr Leu Ala Thr Trp Ala Asp Gly Tyr Glu Arg Arg Pro Ala
81 35 40 45 50
83 aac gca ccg gcg gtc cag ggg caa ccg atc gcc ttt gac gcc tat tcg 303
84 Asn Ala Pro Ala Val Gln Gly Gln Pro Ile Ala Phe Asp Ala Tyr Ser
85 55 60 65
87 gtc gcg cag ctt ttt ggc gac gtc act ggt gcc cgc gtt gcg ggc gtc 351
88 Val Ala Gln Leu Phe Gly Asp Val Thr Gly Ala Arg Val Ala Gly Val
89 70 75 80
91 cag ccg cag cga cac cac ata cgg ccg gtc cgg ttg cgg ggg ccg ttg 399
92 Gln Pro Gln Arg His His Ile Arg Pro Val Arg Leu Arg Gly Pro Leu
93 85 90 95
95 ggt ggg gtt ggg tgc ctc cgt cac ccc agg cag ttc gct ggc tat ttg 447
96 Gly Gly Val Gly Cys Leu Arg His Pro Arg Gln Phe Ala Gly Tyr Leu
97 100 105 110
99 tcg cag tagcgcgacg gcattgtcg atg tot tgg tagctagcat ccggtcgggg 501
100 Ser Gln Met Ser Trp
101 115
103 ggccgctacc agcgcacagc cccggggctcc ccggtccggg tagtgccgct cgagttggtc 561
105 gtggaccagc a atg act gcg acc cgg cga ctt cga aac cgc cac cgg tta 611
106 Met Thr Ala Thr Arg Arg Leu Arg Asn Arg His Arg Leu
107 120 125 130
109 gat tcc ccg act gcg tca tcg cca ggt aaa ccg ccg gca cta acg cca 659
110 Asp Ser Pro Thr Ala Ser Ser Pro Gly Lys Pro Pro Ala Leu Thr Pro
111 135 140 145
113 gca acc aac ccg tgaagaccaa ccaacggcac ctgcgcaggt tgcggctcaa 711
114 Ala Thr Asn Pro
115 150
117 ccgcacatc atg aac tgc tgg att tcg gac tcc ccg tac tct cgc gca gtg 760
118 Met Asn Cys Trp Ile Ser Asp Ser Pro Tyr Ser Arg Ala Val
119 155 160 165
121 cgt gcc cgc gag cct acc gaa gat cgc gtg cat gcg ttc ggc gtg gac 808
122 Arg Ala Arg Glu Pro Thr Glu Asp Arg Val His Ala Phe Gly Val Asp
123 170 175 180
125 cgc aca gca cct gga gtt ggc ggc gcc gag ggc cga gat ggc agg atg 856
126 Arg Thr Ala Pro Gly Val Gly Gly Ala Glu Gly Arg Asp Gly Arg Met
127 185 190 195

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129 acg gat cgt cgg ggg cgg gaa ctc cca ggc cgc cgg acc gtc gca aac 904
130 Thr Asp Arg Arg Gly Arg Glu Leu Pro Gly Arg Arg Thr Val Ala Asn
131 200 205 210
133 ccg tcg caa acc cgt cgc aaa ccg taaggagtca tcc atg aag aca ggc 953
134 Pro Ser Gln Thr Arg Arg Lys Pro Met Lys Thr Gly
135 215 220 225
137 acc gcg acg acg cgg cgc agg ctg ttg gca gta ctg atc gcc ctc gcg 1001
138 Thr Ala Thr Thr Arg Arg Arg Leu Leu Ala Val Leu Ile Ala Leu Ala
139 230 235 240
141 ttg ccg ggg gcc gcc gtt gcg ctg ctg gcc gaa cca tca gcg acc ggc 1049
142 Leu Pro Gly Ala Ala Val Ala Leu Leu Ala Glu Pro Ser Ala Thr Gly
143 245 250 255
145 gcg tcg gac ccg tgc gcg gcc agc gaa gtg gcg agg acg gtc ggt tcg 1097
146 Ala Ser Asp Pro Cys Ala Ala Ser Glu Val Ala Arg Thr Val Gly Ser
147 260 265 270
149 gtc gcc aag tcg atg ggc gac tac ctg gat tca cac cca gag acc aac 1145
150 Val Ala Lys Ser Met Gly Asp Tyr Leu Asp Ser His Pro Glu Thr Asn
151 275 280 285 290
153 cag gtg atg acc gcg gtc ttg cag cag cag gta ggg ccg ggg tcg gtc 1193
154 Gln Val Met Thr Ala Val Leu Gln Gln Gln Val Gly Pro Gly Ser Val
155 295 300 305
157 gca tcg ctg aag gcc cat ttc gag gcg aat ccc aag gtc gca tcg gat 1241
158 Ala Ser Leu Lys Ala His Phe Glu Ala Asn Pro Lys Val Ala Ser Asp
159 310 315 320
161 cc 1243
164 <210> SEQ ID NO: 2
165 <211> LENGTH: 322
166 <212> TYPE: PRT
167 <213> ORGANISM: Mycobacterium tuberculosis
169 <400> SEQUENCE: 2
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171 1 5 10 15
173 Phe Asp Val Pro Leu Tyr Thr Leu Ala Glu Ala Ser Arg Tyr Leu Val
174 20 25 30
176 Val Pro Arg Ala Thr Leu Ala Thr Trp Ala Asp Gly Tyr Glu Arg Arg
177 35 40 45
179 Pro Ala Asn Ala Pro Ala Val Gln Gly Gln Pro Ile Ala Phe Asp Ala
180 50 55 60
182 Tyr Ser Val Ala Gln Leu Phe Gly Asp Val Thr Gly Ala Arg Val Ala
183 65 70 75 80
185 Gly Val Gln Pro Gln Arg His His Ile Arg Pro Val Arg Leu Arg Gly
186 85 90 95
188 Pro Leu Gly Gly Val Gly Cys Leu Arg His Pro Arg Gln Phe Ala Gly
189 100 105 110
191 Tyr Leu Ser Gln Met Ser Trp Met Thr Ala Thr Arg Arg Leu Arg Asn
192 115 120 125
194 Arg His Arg Leu Asp Ser Pro Thr Ala Ser Ser Pro Gly Lys Pro Pro
195 130 135 140
197 Ala Leu Thr Pro Ala Thr Asn Pro Met Asn Cys Trp Ile Ser Asp Ser

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198 145          150          155          160
200 Pro Tyr Ser Arg Ala Val Arg Ala Arg Glu Pro Thr Glu Asp Arg Val
201          165          170          175
203 His Ala Phe Gly Val Asp Arg Thr Ala Pro Gly Val Gly Gly Ala Glu
204          180          185          190
206 Gly Arg Asp Gly Arg Met Thr Asp Arg Arg Gly Arg Glu Leu Pro Gly
207          195          200          205
209 Arg Arg Thr Val Ala Asn Pro Ser Gln Thr Arg Arg Lys Pro Met Lys
210          210          215          220
212 Thr Gly Thr Ala Thr Thr Arg Arg Arg Leu Leu Ala Val Leu Ile Ala
213 225          230          235          240
215 Leu Ala Leu Pro Gly Ala Ala Val Ala Leu Leu Ala Glu Pro Ser Ala
216          245          250          255
218 Thr Gly Ala Ser Asp Pro Cys Ala Ala Ser Glu Val Ala Arg Thr Val
219          260          265          270
221 Gly Ser Val Ala Lys Ser Met Gly Asp Tyr Leu Asp Ser His Pro Glu
222          275          280          285
224 Thr Asn Gln Val Met Thr Ala Val Leu Gln Gln Gln Val Gly Pro Gly
225          290          295          300
227 Ser Val Ala Ser Leu Lys Ala His Phe Glu Ala Asn Pro Lys Val Ala
228 305          310          315          320
230 Ser Asp
233 <210> SEQ ID NO: 3
234 <211> LENGTH: 6
235 <212> TYPE: PRT
236 <213> ORGANISM: Mycobacterium tuberculosis
238 <400> SEQUENCE: 3
239 Met Val Val Gly Met Thr
240 1          5
243 <210> SEQ ID NO: 4
244 <211> LENGTH: 110
245 <212> TYPE: PRT
246 <213> ORGANISM: Mycobacterium tuberculosis
248 <400> SEQUENCE: 4
249 Met Ala Gly Asp Gln Glu Leu Glu Leu Arg Phe Asp Val Pro Leu Tyr
250 1          5          10          15
252 Thr Leu Ala Glu Ala Ser Arg Tyr Leu Val Val Pro Arg Ala Thr Leu
253          20          25          30
255 Ala Thr Trp Ala Asp Gly Tyr Glu Arg Arg Pro Ala Asn Ala Pro Ala
256          35          40          45
258 Val Gln Gly Gln Pro Ile Ala Phe Asp Ala Tyr Ser Val Ala Gln Leu
259          50          55          60
261 Phe Gly Asp Val Thr Gly Ala Arg Val Ala Gly Val Gln Pro Gln Arg
262 65          70          75          80
264 His His Ile Arg Pro Val Arg Leu Arg Gly Pro Leu Gly Gly Val Gly
265          85          90          95
267 Cys Leu Arg His Pro Arg Gln Phe Ala Gly Tyr Leu Ser Gln
268          100          105          110
271 <210> SEQ ID NO: 5

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272 <211> LENGTH: 33
273 <212> TYPE: PRT
274 <213> ORGANISM: Mycobacterium tuberculosis
276 <400> SEQUENCE: 5
277 Met Thr Ala Thr Arg Arg Leu Arg Asn Arg His Arg Leu Asp Ser Pro
278   1           5           10           15
280 Thr Ala Ser Ser Pro Gly Lys Pro Pro Ala Leu Thr Pro Ala Thr Asn
281           20           25           30
283 Pro
286 <210> SEQ ID NO: 6
287 <211> LENGTH: 70
288 <212> TYPE: PRT
289 <213> ORGANISM: Mycobacterium tuberculosis
291 <400> SEQUENCE: 6
292 Met Asn Cys Trp Ile Ser Asp Ser Pro Tyr Ser Arg Ala Val Arg Ala
293   1           5           10           15
295 Arg Glu Pro Thr Glu Asp Arg Val His Ala Phe Gly Val Asp Arg Thr
296           20           25           30
298 Ala Pro Gly Val Gly Gly Ala Glu Gly Arg Asp Gly Arg Met Thr Asp
299           35           40           45
301 Arg Arg Gly Arg Glu Leu Pro Gly Arg Arg Thr Val Ala Asn Pro Ser
302           50           55           60
304 Gln Thr Arg Arg Lys Pro
305   65           70
308 <210> SEQ ID NO: 7
309 <211> LENGTH: 100
310 <212> TYPE: PRT
311 <213> ORGANISM: Mycobacterium tuberculosis
313 <400> SEQUENCE: 7
314 Met Lys Thr Gly Thr Ala Thr Thr Arg Arg Arg Leu Leu Ala Val Leu
315   1           5           10           15
317 Ile Ala Leu Ala Leu Pro Gly Ala Ala Val Ala Leu Leu Ala Glu Pro
318           20           25           30
320 Ser Ala Thr Gly Ala Ser Asp Pro Cys Ala Ala Ser Glu Val Ala Arg
321           35           40           45
323 Thr Val Gly Ser Val Ala Lys Ser Met Gly Asp Tyr Leu Asp Ser His
324           50           55           60
326 Pro Glu Thr Asn Gln Val Met Thr Ala Val Leu Gln Gln Gln Val Gly
327   65           70           75           80
329 Pro Gly Ser Val Ala Ser Leu Lys Ala His Phe Glu Ala Asn Pro Lys
330           85           90           95
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333           100
336 <210> SEQ ID NO: 8
337 <211> LENGTH: 961
338 <212> TYPE: DNA
339 <213> ORGANISM: Mycobacterium tuberculosis
341 <220> FEATURE:
342 <221> NAME/KEY: CDS

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/855,604

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Input Set : D:\37156201.app
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:935; Xaa Pos. 3.

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:8; Line(s) 420,424
Seq#:14; Line(s) 650
Seq#:169; Line(s) 5660
Seq#:177; Line(s) 5811
Seq#:228; Line(s) 7196,7200,7204
Seq#:238; Line(s) 7407,7411
Seq#:290; Line(s) 8869
Seq#:297; Line(s) 9097,9117,9125,9141
Seq#:310; Line(s) 9408,9416
Seq#:347; Line(s) 10644,10648,10656,10660,10664,10668,10672,10676,10680
Seq#:347; Line(s) 10684,10688,10692,10696,10700,10704,10708,10712,10732
Seq#:412; Line(s) 13020,13024
Seq#:463; Line(s) 14779
Seq#:510; Line(s) 16792,16796,16800
Seq#:640; Line(s) 22025
Seq#:702; Line(s) 24419,24431,24435,24439,24443,24455,24459,24463
Seq#:717; Line(s) 24867
Seq#:771; Line(s) 26795,26799
Seq#:784; Line(s) 27150
Seq#:794; Line(s) 27446,27450
Seq#:848; Line(s) 29649,29669,29673,29677,29709,29713
Seq#:864; Line(s) 30193,30245
Seq#:887; Line(s) 31454,31458,31462